Supporting Material

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
RECEPTOR	E_LYS_34	NZ	E_ASP_38	OD1	3.965
RECEPTOR	E_LYS_34	NZ	E_GLU_994	OE2	2.627
RECEPTOR	E_LYS_63	NZ	E_GLU_702	OE1	3.846
RECEPTOR	E_LYS_63	NZ	E_GLU_702	OE2	2.550
RECEPTOR	E_ARG_76	NH1	E_GLU_566	OE2	3.557
RECEPTOR	E_ARG_84	NH2	E_GLU_80	OE1	3.550
RECEPTOR	E_ARG_93	NH1	E_ASP_200	OD1	3.975
RECEPTOR	E_ARG_93	NH1	E_ASP_200	OD2	2.627
RECEPTOR	E_ARG_99	NH1	E_GLU_199	OE1	2.817
RECEPTOR	E_ARG_99	NH2	E_GLU_199	OE1	2.746
RECEPTOR	E_ARG_99	NH2	E_GLU_199	OE2	3.605
RECEPTOR	E_LYS_106	NZ	E_GLU_103	OE1	2.608
RECEPTOR	E_LYS_106	NZ	E_GLU_103	OE2	3.120
RECEPTOR	E_ARG_135	NH1	E_GLU_137	OE2	2.673
RECEPTOR	E_ARG_144	NH2	E_GLU_174	OE2	2.779
RECEPTOR	E_HIS_167	NE2	E_ASP_234	OD2	2.815
RECEPTOR	E_ARG_195	NH1	E_GLU_191	OE2	2.535
RECEPTOR	E_ARG_216	NH2	E_ASP_190	OD1	2.669
RECEPTOR	E_ARG_216	NH2	E_ASP_190	OD2	2.973
RECEPTOR	E_ARG_239	NH1	E_ASP_237	OD1	3.770
RECEPTOR	E_ARG_239	NH1	E_ASP_237	OD2	2.868
RECEPTOR	E_ARG_240	NH2	E_GLU_278	OE1	3.059
RECEPTOR	E_LYS_252	NZ	E_ASP_287	OD1	2.794
RECEPTOR	E_LYS_252	NZ	E_ASP_287	OD2	2.839
RECEPTOR	E_LYS_319	NZ	E_GLU_281	OE1	2.641
RECEPTOR	E_LYS_319	NZ	E_GLU_281	OE2	2.517
RECEPTOR	E_ARG_351	NH2	E_ASP_253	OD2	3.843
RECEPTOR	E_LYS_380	NZ	E_GLU_405	OE1	3.295
RECEPTOR	E_LYS_380	NZ	E_GLU_405	OE2	3.397
RECEPTOR	E_LYS_381	NZ	E_ASP_379	OD2	2.559
RECEPTOR	E_ARG_383	NH1	E_GLU_1054	OE1	2.888
RECEPTOR	E_ARG_383	NH1	E_GLU_1054	OE2	3.925
RECEPTOR	E_ARG_383	NH2	E_GLU_1054	OE1	2.686
RECEPTOR	E_ARG_383	NH2	E_GLU_1054	OE2	2.723
RECEPTOR	E_ARG_396	NH1	E_GLU_412	OE1	2.752
RECEPTOR	E_ARG_396	NH1	E_GLU_412	OE2	2.717
RECEPTOR	E_ARG_420	NH1	E_ASP_171	OD1	3.769
RECEPTOR	E_ARG_420	NH2	E_ASP_171	OD1	2.750
RECEPTOR	E_ARG_420	NH2	E_ASP_171	OD2	2.677
RECEPTOR	E_ARG_420	NH2	E_ASP_237	OD2	3.814
RECEPTOR	E_ARG_432	NH1	E_GLU_1054	OE1	3.586
RECEPTOR	E_LYS_442	NZ	E_GLU_105	OE1	3.982
RECEPTOR	E_LYS_442	NZ	E_GLU_105	OE2	2.575
RECEPTOR	E_ARG_499	NH1	E_ASP_496	OD1	2.642
RECEPTOR	E_ARG_503	NH2	E_GLU_745	OE2	2.942
RECEPTOR	E_HIS_524	NE2	E_GLU_546	OE1	2.736
RECEPTOR	E_LYS_530	NZ	E_GLU_536	OE1	2.617
RECEPTOR	E_LYS_552	NZ	E_GLU_546	OE2	2.668
RECEPTOR	E_ARG_556	NH1	E_ASP_541	OD1	2.642
RECEPTOR	E_ARG_556	NH1	E_ASP_541	OD2	3.053
RECEPTOR	E_ARG_556	NH2	E_ASP_541	OD1	3.841
RECEPTOR	E_ARG_556	NH2	E_ASP_541	OD2	3.614
RECEPTOR	E_LYS_558	NZ	E_GLU_563	OE1	3.644
RECEPTOR	E_LYS_574	NZ	E_GLU_578	OE1	2.573
RECEPTOR	E_ARG_579	NH2	E_ASP_577	OD2	2.911
RECEPTOR	E_ARG_586	NH1	E_ASP_757	OD1	2.661
RECEPTOR	E_ARG_586	NH1	E_ASP_757	OD2	2.677

RECEPTOR	E_LYS_613	NZ	E_GLU_71	OE1	3.917
RECEPTOR	E_LYS_613	NZ	E_GLU_71	OE2	2.570
RECEPTOR	E_LYS_615	NZ	E_ASP_66	OD1	3.911
RECEPTOR	E_ARG_652	NH2	E_ASP_725	OD1	3.724
RECEPTOR	E_ARG_692	NH2	E_ASP_725	OD2	3.430
RECEPTOR	E_LYS_718	NZ	E_ASP_805	OD1	3.365
RECEPTOR	E_ARG_754	NH1	E_ASP_843	OD1	3.846
RECEPTOR	E_ARG_754	NH2	E_ASP_582	OD1	2.635
RECEPTOR	E_ARG_754	NH2	E_ASP_582	OD2	3.602
RECEPTOR	E_ARG_754	NH2	E_ASP_843	OD1	3.241
RECEPTOR	E_ARG_754	NH2	E_ASP_843	OD2	3.196
RECEPTOR	E_LYS_796	NZ	E_ASP_759	OD1	3.240
RECEPTOR	E_ARG_831	NH1	E_ASP_853	OD1	2.776
RECEPTOR	E_ARG_831	NH1	E_ASP_853	OD2	2.814
RECEPTOR	E_ARG_861	NH1	E_GLU_865	OE1	2.786
RECEPTOR	E_ARG_861	NH2	E_GLU_865	OE1	3.266
RECEPTOR	E_LYS_884	NZ	E_GLU_965	OE1	3.364
RECEPTOR	E_LYS_884	NZ	E_GLU_965	OE2	3.301
RECEPTOR	E_LYS_899	NZ	E_ASP_320	OD1	3.025
RECEPTOR	E_LYS_976	NZ	E_ASP_974	OD1	3.874
RECEPTOR	E_ARG_1039	NH1	E_ASP_541	OD2	2.734
RECEPTOR	E_ARG_1039	NH1	E_ASP_544	OD1	3.406
RECEPTOR	E_ARG_1039	NH1	E_ASP_544	OD2	2.621
RECEPTOR	E_ARG_1039	NH2	E_ASP_544	OD1	2.755
RECEPTOR	E_ARG_1039	NH2	E_ASP_544	OD2	3.588
RECEPTOR	E_ARG_1039	NH2	E_GLU_548	OE1	3.791
RECEPTOR	E_ARG_1041	NH1	E_ASP_286	OD1	3.301

Table 1: Salt bridging networks within the structural model represented in RECEPTOR.pdb. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

Count	Residue A	Residue B
4	ARG383	GLU1054
4	ARG556	ASP541
4	ARG1039	ASP544
3	ARG754	ASP843
3	ARG99	GLU199
3	ARG420	ASP171
2	LYS319	GLU281
2	LYS106	GLU103
2	LYS380	GLU405
2	ARG93	ASP200
2	LYS884	GLU965
2	ARG754	ASP582
2	LYS252	ASP287
2	ARG396	GLU412
2	LYS613	GLU71
2	LYS442	GLU105
2	ARG861	GLU865
2	ARG831	ASP853
2	LYS63	GLU702
2	ARG586	ASP757
2	ARG216	ASP190
2	ARG239	ASP237
1	LYS718	ASP805
1	ARG1039	GLU548
1	LYS796	ASP759
1	LYS574	GLU578
1	LYS34	GLU994
1	ARG1041	ASP286
1	LYS899	ASP320
1	ARG240	GLU278
1	LYS558	GLU563
1	LYS381	ASP379
1	ARG432	GLU1054
1	ARG144	GLU174
1	ARG84	GLU80
1	LYS530	GLU536
1	ARG1039	ASP541
1	LYS976	ASP974
1	ARG692	ASP725
1	ARG195	GLU191
1	LYS552	GLU546
1	ARG499	ASP496
1	ARG503	GLU745
1	ARG351	ASP253
1	ARG579	ASP577
1	ARG652	ASP725
1	LYS615	ASP66
1	ARG76	GLU566
1	ARG135	GLU137
1	HIS524	GLU546
1	LYS34	ASP38
1	ARG420	ASP237
1	HIS167	ASP234

Table 2: Counting of side chain salt bridging networks within the structural model represented in RECEPTOR.pdb. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH(°)$
RECEPTOR.PDB	O, E_PRO_30	N, E_LYS_34	H, E_LYS_34	2.94	1.98	14.21
RECEPTOR.PDB	O, E_VAL_31	N, E_SER_35	H, E_SER_35	2.91	1.91	6.86
RECEPTOR.PDB	O, E_ILE_33	N, E_VAL_37	H, E_VAL_37	2.73	1.81	19.33
RECEPTOR.PDB	O, E_VAL_37	N, E_MET_40	H, E_MET_40	2.91	1.91	4.20
RECEPTOR.PDB	O, E_GLN_41	N, E_VAL_45	H, E_VAL_45	2.83	1.83	4.69
RECEPTOR.PDB	O, E_GLU_42	N, E_THR_46	H, E_THR_46	2.95	1.98	13.80
RECEPTOR.PDB	O, E_ASP_43	N, E_LEU_47	H, E_LEU_47	2.93	1.95	11.52
RECEPTOR.PDB	O, E_LEU_44	N, E_ALA_48	H, E_ALA_48	2.79	1.81	10.84
RECEPTOR.PDB	O, E_VAL_45	N, E_LYS_49	H, E_LYS_49	2.72	1.73	9.56
RECEPTOR.PDB	OH, E_TYR_761	NZ, E_LYS_49	HZ3, E_LYS_49	2.82	1.87	15.75
RECEPTOR.PDB	O, E_ALA_48	OG, E_SER_52	HG, E_SER_52	2.87	2.04	25.07
RECEPTOR.PDB	O, E_GLY_53	N, E_LEU_57	H, E_LEU_57	2.92	1.92	7.58
RECEPTOR.PDB	O, E_THR_55	N, E_ASP_59	H, E_ASP_59	2.89	1.91	12.19
RECEPTOR.PDB	O, E_ASP_59	N, E_LYS_63	H, E_LYS_63	2.72	1.90	29.02
RECEPTOR.PDB	OE2, E_GLU_702	NZ, E_LYS_63	HZ3, E_LYS_63	2.55	1.67	23.67
RECEPTOR.PDB	OE1, E_GLU_702	OH, E_TYR_64	HH, E_TYR_64	2.58	1.69	17.39
RECEPTOR.PDB	O, E_GLU_62	NE2, E_GLN_65	HE21, E_GLN_65	2.85	1.89	14.40
RECEPTOR.PDB	O, E_TYR_64	N, E_ASP_66	H, E_ASP_66	2.62	1.80	28.10
RECEPTOR.PDB	O, E_TYR_61	OH, E_TYR_68	HH, E_TYR_68	2.78	1.86	12.52
RECEPTOR.PDB	O, E_PHE_609	N, E_ASN_73	H, E_ASN_73	2.74	1.88	25.24
RECEPTOR.PDB	O, E_SER_608	ND2, E_ASN_73	HD21, E_ASN_73	2.83	1.85	11.46
RECEPTOR.PDB	O, E_GLY_565	NH1, E_ARG_76	HH12, E_ARG_76	2.92	1.98	17.36
RECEPTOR.PDB	O, E_TRP_590	NH2, E_ARG_76	HH22, E_ARG_76	2.82	1.86	13.91
RECEPTOR.PDB	O, E_ASN_74	N, E_LEU_78	H, E_LEU_78	2.84	1.84	8.14
RECEPTOR.PDB	O, E_GLN_77	N, E_ILE_81	H, E_ILE_81	2.89	1.90	9.77
RECEPTOR.PDB	O, E_VAL_79	N, E_ALA_83	H, E_ALA_83	2.85	1.88	12.75
RECEPTOR.PDB	O, E_ARG_84	N, E_LYS_88	H, E_LYS_88	2.82	1.82	8.28
RECEPTOR.PDB	O, E_ASP_85	N, E_LEU_89	H, E_LEU_89	2.81	1.82	9.70
RECEPTOR.PDB	O, E_ILE_86	N, E_LEU_90	H, E_LEU_90	3.00	2.00	7.43
RECEPTOR.PDB	O, E_GLU_87	N, E_SER_91	H, E_SER_91	2.83	1.85	12.48
RECEPTOR.PDB	O, E_LYS_88	N, E_ASN_92	H, E_ASN_92	2.78	1.79	9.61
RECEPTOR.PDB	O, E_LEU_90	N, E_SER_94	H, E_SER_94	2.92	1.98	17.38
RECEPTOR.PDB	O, E_SER_94	N, E_VAL_98	H, E_VAL_98	2.99	2.03	15.26
RECEPTOR.PDB	OD1, E_ASN_196	NH1, E_ARG_99	HH11, E_ARG_99	2.68	1.70	11.75
RECEPTOR.PDB	O, E_VAL_98	N, E_MET_102	H, E_MET_102	2.98	1.99	9.33
RECEPTOR.PDB	O, E_LEU_100	N, E_ALA_104	H, E_ALA_104	2.90	1.90	8.50
RECEPTOR.PDB	O, E_ALA_101	N, E_GLU_105	H, E_GLU_105	2.94	1.94	5.92
RECEPTOR.PDB	OE1, E_GLU_103	NZ, E_LYS_106	HZ1, E_LYS_106	2.61	1.71	21.86
RECEPTOR.PDB	O, E_GLU_103	N, E_VAL_107	H, E_VAL_107	2.75	1.77	10.40
RECEPTOR.PDB	OD1, E_ASN_181	NE2, E_HIS_111	HE2, E_HIS_111	2.75	1.77	11.13
RECEPTOR.PDB	OD1, E_ASN_184	NE, E_ARG_114	HE, E_ARG_114	2.74	1.86	24.17
RECEPTOR.PDB	O, E_ASN_120	NH1, E_ARG_114	HH12, E_ARG_114	2.89	1.96	18.60
RECEPTOR.PDB	O, E_VAL_166	N, E_ALA_127	H, E_ALA_127	2.74	1.76	11.15
RECEPTOR.PDB	OE2, E_GLU_137	NH1, E_ARG_135	HH11, E_ARG_135	2.67	1.74	17.34
RECEPTOR.PDB	O, E_VAL_122	N, E_GLN_143	H, E_GLN_143	2.89	1.90	10.11
RECEPTOR.PDB	OH, E_TYR_124	NH1, E_ARG_144	HH12, E_ARG_144	2.85	1.98	24.37
RECEPTOR.PDB	OD1, E_ASP_152	N, E_ALA_153	H, E_ALA_153	2.80	1.90	22.54
RECEPTOR.PDB	O, E_PHE_155	N, E_ARG_157	H, E_ARG_157	2.99	2.13	26.07
RECEPTOR.PDB	O, E_PRO_222	NH1, E_ARG_157	HH12, E_ARG_157	2.64	1.81	27.30
RECEPTOR.PDB	O, E_ILE_150	N, E_ILE_159	H, E_ILE_159	2.82	1.82	8.15
RECEPTOR.PDB	O, E_ALA_220	N, E_SER_160	H, E_SER_160	2.73	1.84	23.08
RECEPTOR.PDB	OD2, E_ASP_152	OH, E_TYR_161	HH, E_TYR_161	2.55	1.75	27.20
RECEPTOR.PDB	O, E_TYR_217	N, E_ALA_165	H, E_ALA_165	2.81	2.00	29.85
RECEPTOR.PDB	O, E_ALA_215	N, E_HIS_167	H, E_HIS_167	2.73	1.77	14.30
RECEPTOR.PDB	OD2, E_ASP_234	NE2, E_HIS_167	HE2, E_HIS_167	2.81	1.81	5.73
RECEPTOR.PDB	O, E_SER_176	N, E_LEU_180	H, E_LEU_180	2.91	1.91	7.64
RECEPTOR.PDB	OE2, E_GLU_182	NE1, E_TRP_185	HE1, E_TRP_185	2.71	1.84	24.46

RECEPTOR.PDB	O, E_GLU_182	N, E_THR_186	H, E_THR_186	2.84	1.87	12.70
RECEPTOR.PDB	O, E_LEU_183	OG, E_SER_187	HG, E_SER_187	2.76	1.91	22.46
RECEPTOR.PDB	O, E_LEU_189	N, E_PHE_193	H, E_PHE_193	2.81	1.80	3.11
RECEPTOR.PDB	O, E_GLN_162	NZ, E_LYS_194	HZ3, E_LYS_194	2.70	1.73	13.78
RECEPTOR.PDB	OE2, E_GLU_191	NH1, E_ARG_195	HH11, E_ARG_195	2.53	1.55	9.17
RECEPTOR.PDB	OE1, E_GLN_206	ND2, E_ASN_196	HD21, E_ASN_196	2.66	1.78	22.72
RECEPTOR.PDB	O, E_LYS_194	N, E_ASP_198	H, E_ASP_198	2.88	1.89	10.48
RECEPTOR.PDB	O, E_ASN_196	N, E_ASP_200	H, E_ASP_200	2.84	1.89	15.34
RECEPTOR.PDB	O, E_GLY_489	N, E_VAL_207	H, E_VAL_207	2.95	1.98	13.51
RECEPTOR.PDB	O, E_ARG_216	N, E_PHE_208	H, E_PHE_208	2.88	1.91	12.83
RECEPTOR.PDB	O, E_VAL_487	N, E_GLY_209	H, E_GLY_209	2.77	1.79	12.19
RECEPTOR.PDB	O, E_LEU_214	N, E_SER_210	H, E_SER_210	2.76	1.80	15.49
RECEPTOR.PDB	OE1, E_GLU_182	OG, E_SER_210	HG, E_SER_210	2.55	1.66	17.72
RECEPTOR.PDB	O, E_LEU_485	N, E_ALA_211	H, E_ALA_211	2.81	1.82	8.45
RECEPTOR.PDB	O, E_HIS_167	N, E_ALA_215	H, E_ALA_215	2.92	1.92	4.63
RECEPTOR.PDB	O, E_PHE_208	N, E_ARG_216	H, E_ARG_216	2.96	2.00	14.10
RECEPTOR.PDB	OD1, E_ASP_190	NH2, E_ARG_216	HH21, E_ARG_216	2.67	1.79	23.24
RECEPTOR.PDB	O, E_ALA_165	N, E_TYR_217	H, E_TYR_217	2.95	1.97	11.25
RECEPTOR.PDB	O, E_GLN_206	N, E_TYR_218	H, E_TYR_218	2.94	1.96	12.40
RECEPTOR.PDB	O, E_TYR_161	OH, E_TYR_218	HH, E_TYR_218	2.83	1.95	19.75
RECEPTOR.PDB	O, E_LEU_937	ND2, E_ASN_231	HD21, E_ASN_231	2.83	1.97	25.12
RECEPTOR.PDB	OD1, E_ASP_237	N, E_ARG_239	H, E_ARG_239	2.81	1.86	15.87
RECEPTOR.PDB	OD1, E_ASP_237	NE, E_ARG_239	HE, E_ARG_239	2.70	1.73	13.07
RECEPTOR.PDB	OD2, E_ASP_237	NH1, E_ARG_239	HH11, E_ARG_239	2.87	1.92	16.36
RECEPTOR.PDB	O, E_ALA_211	NH2, E_ARG_239	HH21, E_ARG_239	2.80	1.90	22.39
RECEPTOR.PDB	O, E_ARG_241	N, E_ILE_245	H, E_ILE_245	3.00	2.01	11.16
RECEPTOR.PDB	OD1, E_ASP_287	NZ, E_LYS_252	HZ1, E_LYS_252	2.79	1.89	21.20
RECEPTOR.PDB	O, E_PHE_288	N, E_MET_254	H, E_MET_254	2.76	1.82	17.21
RECEPTOR.PDB	O, E_MET_359	N, E_LEU_257	H, E_LEU_257	2.71	1.73	11.16
RECEPTOR.PDB	O, E_ALA_292	N, E_VAL_258	H, E_VAL_258	2.96	2.14	29.21
RECEPTOR.PDB	O, E_PHE_361	N, E_ASP_259	H, E_ASP_259	3.00	2.02	11.40
RECEPTOR.PDB	OD1, E_ASP_259	N, E_SER_261	H, E_SER_261	2.98	1.99	10.55
RECEPTOR.PDB	O, E_GLY_329	N, E_GLY_262	H, E_GLY_262	2.87	1.94	18.55
RECEPTOR.PDB	O, E_LEU_271	N, E_SER_275	H, E_SER_275	2.94	1.94	7.15
RECEPTOR.PDB	O, E_ILE_272	N, E_VAL_276	H, E_VAL_276	2.89	1.90	8.24
RECEPTOR.PDB	O, E_THR_274	N, E_GLU_278	H, E_GLU_278	2.92	1.92	6.05
RECEPTOR.PDB	O, E_SER_275	N, E_MET_279	H, E_MET_279	2.80	1.85	15.06
RECEPTOR.PDB	O, E_SER_284	N, E_ASP_287	H, E_ASP_287	2.85	1.98	25.32
RECEPTOR.PDB	O, E_LYS_252	N, E_PHE_288	H, E_PHE_288	2.82	1.90	19.45
RECEPTOR.PDB	O, E_VAL_308	N, E_VAL_289	H, E_VAL_289	2.81	1.82	9.70
RECEPTOR.PDB	OE1, E_GLN_343	ND2, E_ASN_290	HD21, E_ASN_290	2.87	1.94	19.14
RECEPTOR.PDB	OD1, E_ASN_290	N, E_VAL_291	H, E_VAL_291	2.77	1.94	28.25
RECEPTOR.PDB	O, E_ILE_256	N, E_ALA_292	H, E_ALA_292	2.79	1.80	8.07
RECEPTOR.PDB	O, E_GLN_299	N, E_SER_293	H, E_SER_293	2.96	1.96	5.44
RECEPTOR.PDB	O, E_VAL_258	N, E_PHE_294	H, E_PHE_294	2.98	2.02	15.24
RECEPTOR.PDB	O, E_ASN_297	N, E_ASN_295	H, E_ASN_295	2.90	1.91	10.82
RECEPTOR.PDB	O, E_LYS_328	ND2, E_ASN_295	HD21, E_ASN_295	2.70	1.78	19.10
RECEPTOR.PDB	O, E_ASN_295	OG, E_SER_296	HG, E_SER_296	2.84	2.03	27.35
RECEPTOR.PDB	O, E_ASN_295	N, E_ASN_297	H, E_ASN_297	2.91	2.05	26.04
RECEPTOR.PDB	OD1, E_ASN_295	NE2, E_GLN_299	HE22, E_GLN_299	2.83	1.86	13.53
RECEPTOR.PDB	O, E_VAL_291	N, E_VAL_301	H, E_VAL_301	3.00	2.02	11.14
RECEPTOR.PDB	O, E_VAL_289	N, E_VAL_308	H, E_VAL_308	2.89	1.89	4.35
RECEPTOR.PDB	OD1, E_ASN_311	N, E_ASN_314	H, E_ASN_314	2.87	1.88	7.89
RECEPTOR.PDB	O, E_LYS_315	N, E_LYS_319	H, E_LYS_319	2.86	1.86	8.32
RECEPTOR.PDB	O, E_LEU_318	N, E_VAL_322	H, E_VAL_322	2.89	1.92	13.27
RECEPTOR.PDB	O, E_VAL_260	N, E_LYS_328	H, E_LYS_328	2.89	1.92	13.72
RECEPTOR.PDB	O, E_TYR_333	N, E_PHE_337	H, E_PHE_337	2.97	1.98	7.79
RECEPTOR.PDB	O, E_LYS_334	N, E_SER_338	H, E_SER_338	2.94	1.97	11.65

RECEPTOR.PDB	O, E_ASN_346	N, E_ASN_348	H, E_ASN_348	2.67	1.76	19.82
RECEPTOR.PDB	OD1, E_ASP_253	N, E_ALA_352	H, E_ALA_352	2.93	2.00	18.26
RECEPTOR.PDB	OD2, E_ASP_253	N, E_ASN_353	H, E_ASN_353	2.71	1.85	25.68
RECEPTOR.PDB	O, E_ARG_383	N, E_ILE_358	H, E_ILE_358	2.91	1.91	6.79
RECEPTOR.PDB	OD1, E_ASP_363	N, E_GLY_364	H, E_GLY_364	2.67	1.78	22.62
RECEPTOR.PDB	O, E_ASP_395	N, E_GLY_365	H, E_GLY_365	2.99	2.10	22.61
RECEPTOR.PDB	OD1, E_ASN_406	ND2, E_ASN_377	HD22, E_ASN_377	2.70	1.74	14.00
RECEPTOR.PDB	O, E_ASN_377	N, E_LYS_380	H, E_LYS_380	2.82	1.89	17.69
RECEPTOR.PDB	O, E_GLU_405	NZ, E_LYS_380	HZ1, E_LYS_380	2.83	1.95	24.20
RECEPTOR.PDB	OD2, E_ASP_379	NZ, E_LYS_381	HZ1, E_LYS_381	2.56	1.75	29.39
RECEPTOR.PDB	O, E_ILE_399	OG1, E_THR_386	HG1, E_THR_386	2.85	1.92	12.47
RECEPTOR.PDB	O, E_LEU_360	N, E_PHE_387	H, E_PHE_387	2.93	2.00	19.08
RECEPTOR.PDB	O, E_TYR_411	N, E_SER_388	H, E_SER_388	2.97	2.00	13.12
RECEPTOR.PDB	O, E_ASP_363	OG, E_SER_388	HG, E_SER_388	2.96	2.08	19.68
RECEPTOR.PDB	O, E_THR_362	N, E_VAL_389	H, E_VAL_389	2.95	2.07	24.20
RECEPTOR.PDB	O, E_ILE_413	N, E_GLY_390	H, E_GLY_390	2.77	1.79	10.85
RECEPTOR.PDB	ND1, E_HIS_392	N, E_TYR_394	H, E_TYR_394	2.99	2.13	26.24
RECEPTOR.PDB	OD1, E_ASP_395	N, E_GLY_397	H, E_GLY_397	2.81	1.81	6.94
RECEPTOR.PDB	O, E_GLN_400	N, E_CYS_404	H, E_CYS_404	2.96	1.97	8.24
RECEPTOR.PDB	O, E_TRP_401	N, E_GLU_405	H, E_GLU_405	2.95	1.97	10.98
RECEPTOR.PDB	O, E_MET_402	ND2, E_ASN_406	HD21, E_ASN_406	2.75	1.77	11.21
RECEPTOR.PDB	OE2, E_GLU_412	OH, E_TYR_410	HH, E_TYR_410	2.72	1.80	13.73
RECEPTOR.PDB	O, E_SER_388	N, E_ILE_413	H, E_ILE_413	2.89	1.90	10.80
RECEPTOR.PDB	OD1, E_ASP_171	NH2, E_ARG_420	HH22, E_ARG_420	2.75	1.83	19.88
RECEPTOR.PDB	O, E_ILE_419	OG1, E_THR_423	HG1, E_THR_423	2.99	2.18	27.12
RECEPTOR.PDB	OD2, E_ASP_237	NE2, E_GLN_424	HE22, E_GLN_424	2.98	1.97	5.44
RECEPTOR.PDB	O, E_LEU_427	N, E_GLY_431	H, E_GLY_431	2.77	1.89	24.47
RECEPTOR.PDB	O, E_ASP_439	N, E_LYS_442	H, E_LYS_442	2.97	2.00	14.33
RECEPTOR.PDB	OE2, E_GLU_105	NZ, E_LYS_442	HZ1, E_LYS_442	2.57	1.75	28.10
RECEPTOR.PDB	O, E_THR_461	N, E_THR_447	H, E_THR_447	2.92	1.92	6.18
RECEPTOR.PDB	O, E_TYR_450	N, E_VAL_459	H, E_VAL_459	2.77	1.76	3.87
RECEPTOR.PDB	O, E_VAL_492	N, E_ILE_460	H, E_ILE_460	2.94	1.94	7.11
RECEPTOR.PDB	OD1, E_ASP_491	OG1, E_THR_461	HG1, E_THR_461	2.98	2.09	17.09
RECEPTOR.PDB	O, E_VAL_490	N, E_GLY_462	H, E_GLY_462	2.93	1.96	13.01
RECEPTOR.PDB	O, E_GLN_445	N, E_THR_463	H, E_THR_463	2.81	1.92	22.12
RECEPTOR.PDB	O, E_MET_488	N, E_LEU_464	H, E_LEU_464	2.94	1.94	8.70
RECEPTOR.PDB	O, E_GLY_486	N, E_VAL_466	H, E_VAL_466	2.89	1.89	6.33
RECEPTOR.PDB	OE2, E_GLU_105	N, E_PHE_467	H, E_PHE_467	2.85	1.85	7.28
RECEPTOR.PDB	O, E_GLY_471	N, E_ASN_475	H, E_ASN_475	2.94	2.10	27.64
RECEPTOR.PDB	OE1, E_GLU_474	N, E_LYS_476	H, E_LYS_476	2.88	2.02	25.61
RECEPTOR.PDB	O, E_ASN_468	ND2, E_ASN_481	HD21, E_ASN_481	2.84	1.85	9.49
RECEPTOR.PDB	OG1, E_THR_470	ND2, E_ASN_481	HD22, E_ASN_481	2.91	1.92	7.62
RECEPTOR.PDB	O, E_VAL_466	N, E_LEU_485	H, E_LEU_485	2.75	1.87	23.86
RECEPTOR.PDB	O, E_GLY_209	N, E_VAL_487	H, E_VAL_487	2.79	1.81	11.00
RECEPTOR.PDB	O, E_LEU_464	N, E_MET_488	H, E_MET_488	2.89	1.89	4.58
RECEPTOR.PDB	O, E_VAL_207	N, E_GLY_489	H, E_GLY_489	2.90	1.89	5.37
RECEPTOR.PDB	O, E_ILE_460	N, E_VAL_492	H, E_VAL_492	2.80	1.79	4.15
RECEPTOR.PDB	O, E_ILE_497	N, E_LEU_500	H, E_LEU_500	2.97	2.02	16.21
RECEPTOR.PDB	O, E_CYS_507	N, E_GLY_510	H, E_GLY_510	2.84	1.89	15.28
RECEPTOR.PDB	O, E_ALA_601	N, E_PHE_513	H, E_PHE_513	2.80	1.82	11.12
RECEPTOR.PDB	O, E_SER_599	N, E_ILE_515	H, E_ILE_515	2.88	2.05	28.50
RECEPTOR.PDB	O, E_TYR_520	N, E_ASP_516	H, E_ASP_516	2.97	1.97	8.44
RECEPTOR.PDB	OD2, E_ASP_285	OH, E_TYR_520	HH, E_TYR_520	2.54	1.72	25.96
RECEPTOR.PDB	O, E_LEU_540	N, E_VAL_521	H, E_VAL_521	2.92	1.92	8.74
RECEPTOR.PDB	OE1, E_GLU_546	NE2, E_HIS_524	HE2, E_HIS_524	2.74	1.76	12.33
RECEPTOR.PDB	OE1, E_GLN_889	N, E_GLN_528	H, E_GLN_528	2.98	2.04	17.54
RECEPTOR.PDB	OE1, E_GLU_536	NZ, E_LYS_530	HZ1, E_LYS_530	2.62	1.79	27.88
RECEPTOR.PDB	OE1, E_GLU_536	OG, E_SER_534	HG, E_SER_534	2.51	1.58	10.42

RECEPTOR.PDB	O, E_VAL_449	N, E_VAL_538	H, E_VAL_538	2.80	1.80	6.01
RECEPTOR.PDB	OE2, E_GLU_546	NZ, E_LYS_552	HZ1, E_LYS_552	2.67	1.71	15.03
RECEPTOR.PDB	O, E_LYS_552	N, E_ARG_556	H, E_ARG_556	2.83	1.84	9.88
RECEPTOR.PDB	O, E_VAL_553	N, E_ASN_557	H, E_ASN_557	2.92	1.94	10.47
RECEPTOR.PDB	O, E_TYR_588	N, E_LYS_567	H, E_LYS_567	2.76	1.86	22.33
RECEPTOR.PDB	O, E_ARG_586	N, E_PHE_569	H, E_PHE_569	2.95	1.96	10.72
RECEPTOR.PDB	O, E_ASP_582	N, E_VAL_573	H, E_VAL_573	2.79	1.79	7.32
RECEPTOR.PDB	OE1, E_GLU_578	NZ, E_LYS_574	HZ1, E_LYS_574	2.57	1.76	28.91
RECEPTOR.PDB	OE1, E_GLN_966	NZ, E_LYS_574	HZ3, E_LYS_574	2.63	1.76	24.11
RECEPTOR.PDB	O, E_TYR_580	N, E_SER_575	H, E_SER_575	2.98	1.99	7.13
RECEPTOR.PDB	O, E_ASP_577	N, E_ARG_579	H, E_ARG_579	2.69	1.78	20.43
RECEPTOR.PDB	OD2, E_ASP_577	NE, E_ARG_579	HE, E_ARG_579	2.56	1.59	12.49
RECEPTOR.PDB	O, E_VAL_573	N, E_ASP_582	H, E_ASP_582	2.94	1.94	7.31
RECEPTOR.PDB	O, E_PHE_569	N, E_ARG_586	H, E_ARG_586	2.94	1.93	3.72
RECEPTOR.PDB	OD1, E_ASP_757	NH1, E_ARG_586	HH11, E_ARG_586	2.66	1.76	21.42
RECEPTOR.PDB	O, E_LEU_604	N, E_THR_587	H, E_THR_587	2.83	1.82	0.75
RECEPTOR.PDB	O, E_LYS_567	N, E_TYR_588	H, E_TYR_588	2.75	1.76	8.86
RECEPTOR.PDB	O, E_LEU_600	N, E_THR_591	H, E_THR_591	2.93	1.99	17.61
RECEPTOR.PDB	O, E_TYR_598	N, E_VAL_593	H, E_VAL_593	2.89	1.95	16.88
RECEPTOR.PDB	O, E_ILE_515	N, E_SER_599	H, E_SER_599	2.98	2.00	11.96
RECEPTOR.PDB	O, E_THR_591	OG, E_SER_599	HG, E_SER_599	2.98	2.05	11.86
RECEPTOR.PDB	O, E_THR_591	N, E_LEU_600	H, E_LEU_600	2.88	1.88	3.22
RECEPTOR.PDB	O, E_PHE_513	N, E_ALA_601	H, E_ALA_601	2.73	1.75	10.11
RECEPTOR.PDB	O, E_THR_589	N, E_LEU_602	H, E_LEU_602	2.84	1.90	16.63
RECEPTOR.PDB	O, E_TYR_511	N, E_VAL_603	H, E_VAL_603	2.79	1.78	4.08
RECEPTOR.PDB	O, E_THR_587	N, E_LEU_604	H, E_LEU_604	2.97	1.98	7.96
RECEPTOR.PDB	O, E_PRO_605	OG, E_SER_608	HG, E_SER_608	2.97	2.10	20.38
RECEPTOR.PDB	O, E_GLU_71	N, E_TYR_611	H, E_TYR_611	2.83	1.83	6.96
RECEPTOR.PDB	OE2, E_GLU_71	NZ, E_LYS_613	HZ2, E_LYS_613	2.57	1.73	26.74
RECEPTOR.PDB	O, E_LEU_67	N, E_LYS_615	H, E_LYS_615	2.92	1.97	15.86
RECEPTOR.PDB	O, E_GLU_618	N, E_GLN_622	H, E_GLN_622	2.98	1.97	1.44
RECEPTOR.PDB	O, E_ILE_616	NE2, E_GLN_622	HE21, E_GLN_622	2.86	1.92	17.44
RECEPTOR.PDB	O, E_LEU_694	NZ, E_LYS_627	HZ3, E_LYS_627	2.79	1.96	28.62
RECEPTOR.PDB	O, E_ARG_624	N, E_GLY_628	H, E_GLY_628	2.92	1.94	11.86
RECEPTOR.PDB	O, E_LYS_637	N, E_ASN_640	H, E_ASN_640	2.84	1.95	22.87
RECEPTOR.PDB	O, E_VAL_731	N, E_TYR_646	H, E_TYR_646	2.83	1.95	24.01
RECEPTOR.PDB	O, E_THR_729	N, E_PHE_648	H, E_PHE_648	2.80	1.84	14.21
RECEPTOR.PDB	O, E_ALA_650	N, E_ARG_652	H, E_ARG_652	2.79	1.93	25.65
RECEPTOR.PDB	O, E_ALA_650	OH, E_TYR_654	HH, E_TYR_654	2.78	1.85	12.09
RECEPTOR.PDB	O, E_SER_661	N, E_ASN_663	H, E_ASN_663	2.90	2.02	23.80
RECEPTOR.PDB	O, E_ASN_664	N, E_LEU_668	H, E_LEU_668	2.85	1.86	7.92
RECEPTOR.PDB	O, E_PHE_667	N, E_PHE_671	H, E_PHE_671	2.75	1.75	7.86
RECEPTOR.PDB	O, E_LEU_668	N, E_ASN_672	H, E_ASN_672	2.90	2.04	25.85
RECEPTOR.PDB	O, E_LEU_669	N, E_GLU_673	H, E_GLU_673	2.77	1.79	11.95
RECEPTOR.PDB	O, E_GLU_673	N, E_ARG_677	H, E_ARG_677	2.94	1.93	6.05
RECEPTOR.PDB	O, E_THR_687	N, E_ASN_691	H, E_ASN_691	2.94	2.06	24.65
RECEPTOR.PDB	O, E_ILE_616	ND2, E_ASN_691	HD22, E_ASN_691	2.84	1.90	17.72
RECEPTOR.PDB	O, E_ASP_688	N, E_ARG_692	H, E_ARG_692	2.93	1.96	13.13
RECEPTOR.PDB	O, E_ASN_691	N, E_LEU_695	H, E_LEU_695	2.91	1.94	12.22
RECEPTOR.PDB	O, E_ARG_692	N, E_ASP_696	H, E_ASP_696	2.94	1.95	8.60
RECEPTOR.PDB	O, E_ILE_693	N, E_ALA_697	H, E_ALA_697	2.90	1.95	16.21
RECEPTOR.PDB	O, E_ASP_696	N, E_THR_700	H, E_THR_700	2.84	1.85	9.53
RECEPTOR.PDB	O, E_LYS_627	ND2, E_ASN_701	HD21, E_ASN_701	2.85	1.97	23.76
RECEPTOR.PDB	O, E_ASN_701	N, E_GLN_705	H, E_GLN_705	2.78	1.77	2.84
RECEPTOR.PDB	OE1, E_GLU_643	NE2, E_GLN_705	HE22, E_GLN_705	3.00	2.13	25.92
RECEPTOR.PDB	O, E_GLU_702	N, E_ASN_706	H, E_ASN_706	2.85	1.90	16.78
RECEPTOR.PDB	O, E_THR_50	OH, E_TYR_707	HH, E_TYR_707	2.57	1.78	28.32
RECEPTOR.PDB	O, E_LEU_703	N, E_TRP_708	H, E_TRP_708	2.99	2.02	12.77

RECEPTOR.PDB	O, E_SER_52	NE1, E_TRP_708	HE1, E_TRP_708	2.77	1.84	17.38
RECEPTOR.PDB	O, E_LYS_803	N, E_LYS_718	H, E_LYS_718	2.88	1.94	17.63
RECEPTOR.PDB	O, E_VAL_799	N, E_VAL_723	H, E_VAL_723	2.89	1.97	18.85
RECEPTOR.PDB	OD1, E_ASP_696	OG1, E_THR_724	HG1, E_THR_724	2.66	1.75	14.16
RECEPTOR.PDB	O, E_THR_700	NH2, E_ARG_730	HH21, E_ARG_730	2.99	2.09	22.40
RECEPTOR.PDB	O, E_ARG_720	N, E_TYR_732	H, E_TYR_732	2.93	1.99	18.01
RECEPTOR.PDB	OD1, E_ASN_743	N, E_GLU_745	H, E_GLU_745	2.86	1.86	8.97
RECEPTOR.PDB	O, E_LEU_506	OH, E_TYR_747	HH, E_TYR_747	2.63	1.79	24.04
RECEPTOR.PDB	O, E_GLU_745	N, E_GLU_748	H, E_GLU_748	2.89	1.92	13.65
RECEPTOR.PDB	OE1, E_GLN_576	NZ, E_LYS_753	HZ1, E_LYS_753	2.60	1.70	21.45
RECEPTOR.PDB	OD2, E_ASP_582	NE, E_ARG_754	HE, E_ARG_754	2.70	1.71	8.99
RECEPTOR.PDB	OD1, E_ASP_582	NH2, E_ARG_754	HH21, E_ARG_754	2.64	1.67	13.76
RECEPTOR.PDB	O, E_PHE_751	OG, E_SER_755	HG, E_SER_755	2.91	1.99	13.42
RECEPTOR.PDB	O, E_SER_783	N, E_VAL_762	H, E_VAL_762	2.96	1.99	12.97
RECEPTOR.PDB	O, E_MET_781	N, E_THR_764	H, E_THR_764	2.77	1.80	13.04
RECEPTOR.PDB	OE1, E_GLU_777	N, E_ALA_775	H, E_ALA_775	2.91	1.99	20.12
RECEPTOR.PDB	O, E_ILE_802	N, E_VAL_782	H, E_VAL_782	2.87	1.88	9.44
RECEPTOR.PDB	O, E_VAL_762	N, E_SER_783	H, E_SER_783	2.86	1.88	11.33
RECEPTOR.PDB	O, E_VAL_800	N, E_LYS_784	H, E_LYS_784	2.97	1.99	11.52
RECEPTOR.PDB	O, E_ALA_798	N, E_VAL_786	H, E_VAL_786	2.72	1.75	11.96
RECEPTOR.PDB	OE2, E_GLU_62	N, E_TYR_789	H, E_TYR_789	2.72	1.72	7.90
RECEPTOR.PDB	O, E_LEU_756	NZ, E_LYS_796	HZ3, E_LYS_796	2.75	1.79	13.40
RECEPTOR.PDB	O, E_VAL_723	N, E_VAL_799	H, E_VAL_799	2.79	1.80	7.60
RECEPTOR.PDB	O, E_VAL_782	N, E_ILE_802	H, E_ILE_802	2.85	1.88	13.33
RECEPTOR.PDB	O, E_ALA_719	N, E_LYS_803	H, E_LYS_803	2.78	1.82	14.25
RECEPTOR.PDB	O, E_ILE_780	N, E_ILE_804	H, E_ILE_804	2.73	1.72	4.35
RECEPTOR.PDB	O, E_GLY_716	N, E_ASP_805	H, E_ASP_805	2.85	1.85	5.05
RECEPTOR.PDB	OD2, E_ASP_805	N, E_SER_808	H, E_SER_808	2.82	1.84	9.38
RECEPTOR.PDB	OD2, E_ASP_43	ND2, E_ASN_812	HD21, E_ASN_812	2.81	1.88	17.56
RECEPTOR.PDB	O, E_ILE_810	N, E_THR_814	H, E_THR_814	2.80	1.80	7.77
RECEPTOR.PDB	O, E_GLU_811	N, E_LYS_815	H, E_LYS_815	2.99	2.03	15.74
RECEPTOR.PDB	OG, E_SER_833	N, E_LYS_830	H, E_LYS_830	2.93	2.06	25.00
RECEPTOR.PDB	O, E_LYS_830	OG, E_SER_833	HG, E_SER_833	2.52	1.74	28.44
RECEPTOR.PDB	O, E_MET_849	N, E_ILE_840	H, E_ILE_840	2.95	1.96	9.06
RECEPTOR.PDB	O, E_ARG_861	N, E_LEU_847	H, E_LEU_847	2.83	1.83	6.32
RECEPTOR.PDB	O, E_LEU_847	N, E_GLY_860	H, E_GLY_860	2.76	1.80	14.76
RECEPTOR.PDB	O, E_GLY_845	N, E_PHE_863	H, E_PHE_863	3.00	2.04	14.62
RECEPTOR.PDB	O, E_MET_870	N, E_LEU_874	H, E_LEU_874	2.96	2.04	20.42
RECEPTOR.PDB	OD1, E_ASN_973	OG, E_SER_878	HG, E_SER_878	2.88	2.01	20.71
RECEPTOR.PDB	O, E_PHE_970	N, E_ALA_881	H, E_ALA_881	2.90	2.00	21.52
RECEPTOR.PDB	O, E_GLN_966	N, E_SER_885	H, E_SER_885	2.83	1.89	18.01
RECEPTOR.PDB	O, E_THR_964	N, E_ASP_887	H, E_ASP_887	2.85	1.86	8.46
RECEPTOR.PDB	O, E_GLN_900	N, E_ALA_902	H, E_ALA_902	2.97	2.15	29.30
RECEPTOR.PDB	O, E_GLY_895	NH2, E_ARG_905	HH21, E_ARG_905	2.86	1.89	12.87
RECEPTOR.PDB	O, E_ILE_915	N, E_GLN_917	H, E_GLN_917	2.96	2.13	28.49
RECEPTOR.PDB	O, E_SER_890	N, E_CYS_962	H, E_CYS_962	2.88	1.91	13.45
RECEPTOR.PDB	OG, E_SER_890	OG1, E_THR_964	HG1, E_THR_964	2.99	2.05	9.54
RECEPTOR.PDB	O, E_SER_885	N, E_GLN_966	H, E_GLN_966	2.79	1.80	7.89
RECEPTOR.PDB	O, E_ALA_881	N, E_PHE_970	H, E_PHE_970	2.92	1.96	15.05
RECEPTOR.PDB	O, E_ASP_974	NZ, E_LYS_976	HZ2, E_LYS_976	2.99	2.15	27.62
RECEPTOR.PDB	O, E_VAL_993	N, E_PHE_978	H, E_PHE_978	2.90	1.92	11.53
RECEPTOR.PDB	O, E_ARG_989	N, E_LEU_982	H, E_LEU_982	2.95	1.97	12.16
RECEPTOR.PDB	O, E_LEU_982	N, E_ARG_989	H, E_ARG_989	2.90	2.00	22.13
RECEPTOR.PDB	O, E_PHE_978	N, E_VAL_993	H, E_VAL_993	2.94	1.96	11.10

Table 3: The side chain and main chain hydrogen bonding networks within the structural model represented in RECEPTOR.pdb. In this table, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
RECEPTOR.PDB	OH, E_TYR_761	NZ, E_LYS_49	HZ3, E_LYS_49	2.82	1.87	15.75
RECEPTOR.PDB	OE2, E_GLU_702	NZ, E_LYS_63	HZ3, E_LYS_63	2.55	1.67	23.67
RECEPTOR.PDB	OE1, E_GLU_702	OH, E_TYR_64	HH, E_TYR_64	2.58	1.69	17.39
RECEPTOR.PDB	OD1, E_ASN_196	NH1, E_ARG_99	HH11, E_ARG_99	2.68	1.70	11.75
RECEPTOR.PDB	OE1, E_GLU_103	NZ, E_LYS_106	HZ1, E_LYS_106	2.61	1.71	21.86
RECEPTOR.PDB	OD1, E_ASN_181	NE2, E_HIS_111	HE2, E_HIS_111	2.75	1.77	11.13
RECEPTOR.PDB	OD1, E_ASN_184	NE, E_ARG_114	HE, E_ARG_114	2.74	1.86	24.17
RECEPTOR.PDB	OE2, E_GLU_137	NH1, E_ARG_135	HH11, E_ARG_135	2.67	1.74	17.34
RECEPTOR.PDB	OH, E_TYR_124	NH1, E_ARG_144	HH12, E_ARG_144	2.85	1.98	24.37
RECEPTOR.PDB	OD2, E_ASP_152	OH, E_TYR_161	HH, E_TYR_161	2.55	1.75	27.20
RECEPTOR.PDB	OD2, E_ASP_234	NE2, E_HIS_167	HE2, E_HIS_167	2.81	1.81	5.73
RECEPTOR.PDB	OE2, E_GLU_182	NE1, E_TRP_185	HE1, E_TRP_185	2.71	1.84	24.46
RECEPTOR.PDB	OE2, E_GLU_191	NH1, E_ARG_195	HH11, E_ARG_195	2.53	1.55	9.17
RECEPTOR.PDB	OE1, E_GLN_206	ND2, E_ASN_196	HD21, E_ASN_196	2.66	1.78	22.72
RECEPTOR.PDB	OE1, E_GLU_182	OG, E_SER_210	HG, E_SER_210	2.55	1.66	17.72
RECEPTOR.PDB	OD1, E_ASP_190	NH2, E_ARG_216	HH21, E_ARG_216	2.67	1.79	23.24
RECEPTOR.PDB	OD1, E_ASP_237	NE, E_ARG_239	HE, E_ARG_239	2.70	1.73	13.07
RECEPTOR.PDB	OD2, E_ASP_237	NH1, E_ARG_239	HH11, E_ARG_239	2.87	1.92	16.36
RECEPTOR.PDB	OD1, E_ASP_287	NZ, E_LYS_252	HZ1, E_LYS_252	2.79	1.89	21.20
RECEPTOR.PDB	OE1, E_GLN_343	ND2, E_ASN_290	HD21, E_ASN_290	2.87	1.94	19.14
RECEPTOR.PDB	OD1, E_ASN_295	NE2, E_GLN_299	HE22, E_GLN_299	2.83	1.86	13.53
RECEPTOR.PDB	OD1, E_ASN_406	ND2, E_ASN_377	HD22, E_ASN_377	2.70	1.74	14.00
RECEPTOR.PDB	OD2, E_ASP_379	NZ, E_LYS_381	HZ1, E_LYS_381	2.56	1.75	29.39
RECEPTOR.PDB	OE2, E_GLU_412	OH, E_TYR_410	HH, E_TYR_410	2.72	1.80	13.73
RECEPTOR.PDB	OD1, E_ASP_171	NH2, E_ARG_420	HH22, E_ARG_420	2.75	1.83	19.88
RECEPTOR.PDB	OD2, E_ASP_237	NE2, E_GLN_424	HE22, E_GLN_424	2.98	1.97	5.44
RECEPTOR.PDB	OE2, E_GLU_105	NZ, E_LYS_442	HZ1, E_LYS_442	2.57	1.75	28.10
RECEPTOR.PDB	OD1, E_ASP_491	OG1, E_THR_461	HG1, E_THR_461	2.98	2.09	17.09
RECEPTOR.PDB	OG1, E_THR_470	ND2, E_ASN_481	HD22, E_ASN_481	2.91	1.92	7.62
RECEPTOR.PDB	OD2, E_ASP_285	OH, E_TYR_520	HH, E_TYR_520	2.54	1.72	25.96
RECEPTOR.PDB	OE1, E_GLU_546	NE2, E_HIS_524	HE2, E_HIS_524	2.74	1.76	12.33
RECEPTOR.PDB	OE1, E_GLU_536	NZ, E_LYS_530	HZ1, E_LYS_530	2.62	1.79	27.88
RECEPTOR.PDB	OE1, E_GLU_536	OG, E_SER_534	HG, E_SER_534	2.51	1.58	10.42
RECEPTOR.PDB	OE2, E_GLU_546	NZ, E_LYS_552	HZ1, E_LYS_552	2.67	1.71	15.03
RECEPTOR.PDB	OE1, E_GLU_578	NZ, E_LYS_574	HZ1, E_LYS_574	2.57	1.76	28.91
RECEPTOR.PDB	OE1, E_GLN_966	NZ, E_LYS_574	HZ3, E_LYS_574	2.63	1.76	24.11
RECEPTOR.PDB	OD2, E_ASP_577	NE, E_ARG_579	HE, E_ARG_579	2.56	1.59	12.49
RECEPTOR.PDB	OD1, E_ASP_757	NH1, E_ARG_586	HH11, E_ARG_586	2.66	1.76	21.42
RECEPTOR.PDB	OE2, E_GLU_71	NZ, E_LYS_613	HZ2, E_LYS_613	2.57	1.73	26.74
RECEPTOR.PDB	OE1, E_GLU_643	NE2, E_GLN_705	HE22, E_GLN_705	3.00	2.13	25.92
RECEPTOR.PDB	OD1, E_ASP_696	OG1, E_THR_724	HG1, E_THR_724	2.66	1.75	14.16
RECEPTOR.PDB	OE1, E_GLN_576	NZ, E_LYS_753	HZ1, E_LYS_753	2.60	1.70	21.45
RECEPTOR.PDB	OD2, E_ASP_582	NE, E_ARG_754	HE, E_ARG_754	2.70	1.71	8.99
RECEPTOR.PDB	OD1, E_ASP_582	NH2, E_ARG_754	HH21, E_ARG_754	2.64	1.67	13.76
RECEPTOR.PDB	OD2, E_ASP_43	ND2, E_ASN_812	HD21, E_ASN_812	2.81	1.88	17.56
RECEPTOR.PDB	OD1, E_ASN_973	OG, E_SER_878	HG, E_SER_878	2.88	2.01	20.71
RECEPTOR.PDB	OG, E_SER_890	OG1, E_THR_964	HG1, E_THR_964	2.99	2.05	9.54

Table 4: The side chain hydrogen bonding networks within the structural model represented in RECEPTOR.pdb. In this table, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).